

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Alessi, Dario R
- (ii) TITLE OF INVENTION: ENZYME
- (iii) NUMBER OF SEQUENCES: 35
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Jaeckle Fleischmann & Mugel, LLP
 - (B) STREET: 39 State Street
 - (C) CITY: Rochester
 - (D) STATE: New York
 - (E) COUNTRY: USA
 - (F) ZIP: 14614-1310
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/943,667
 - (B) FILING DATE: 03-OCT-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: GB 9705462.1
 - (B) FILING DATE: 17-MAR-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: GB 9712826.8
 - (B) FILING DATE: 19-JUN-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: GB 9717253.0
 - (B) FILING DATE: 15-AUG-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Braman, Susan J
 - (B) REGISTRATION NUMBER: 34,103
 - (C) REFERENCE/DOCKET NUMBER: 87792.97R421
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 716-262-3640
 - (B) TELEFAX: 716-262-4133

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 556 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met	Ala	Arg	Thr	Thr	Ser	Gln	Leu	Tyr	Asp	Ala	Val	Pro	Ile	Gln	Ser	
1				5					10					15		
Ser	Val	Val	Leu	Cys	Ser	Cys	Pro	Ser	Pro	Ser	Met	Val	Arg	Thr	Gln	
			20					25					30			
Thr	Glu	Ser	Ser	Thr	Pro	Pro	Gly	Ile	Pro	Gly	Gly	Ser	Arg	Gln	Gly	
			35				40					45				
Pro	Ala	Met	Asp	Gly	Thr	Ala	Ala	Glu	Pro	Arg	Pro	Gly	Ala	Gly	Ser	
	50					55					60					
Leu	Gln	His	Ala	Gln	Pro	Pro	Pro	Gln	Pro	Arg	Lys	Lys	Arg	Pro	Glu	
65					70					75					80	
Asp	Phe	Lys	Phe	Gly	Lys	Ile	Leu	Gly	Glu	Gly	Ser	Phe	Ser	Thr	Val	
				85					90					95		
Val	Leu	Ala	Arg	Glu	Leu	Ala	Thr	Ser	Arg	Glu	Tyr	Ala	Ile	Lys	Ile	
			100					105					110			
Leu	Glu	Lys	Arg	His	Ile	Ile	Lys	Glu	Asn	Lys	Val	Pro	Tyr	Val	Thr	
		115					120					125				
Arg	Glu	Arg	Asp	Val	Met	Ser	Arg	Leu	Asp	His	Pro	Phe	Phe	Val	Lys	
	130					135					140					
Leu	Tyr	Phe	Thr	Phe	Gln	Asp	Asp	Glu	Lys	Leu	Tyr	Phe	Gly	Leu	Ser	
145					150					155					160	
Tyr	Ala	Lys	Asn	Gly	Glu	Leu	Leu	Lys	Tyr	Ile	Arg	Lys	Ile	Gly	Ser	
				165					170					175		
Phe	Asp	Glu	Thr	Cys	Thr	Arg	Phe	Tyr	Thr	Ala	Glu	Ile	Val	Ser	Ala	
			180					185					190			
Leu	Glu	Tyr	Leu	His	Gly	Lys	Gly	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	

195					200					205					
Glu	Asn	Ile	Leu	Leu	Asn	Glu	Asp	Met	His	Ile	Gln	Ile	Thr	Asp	Phe
	210					215					220				
Gly	Thr	Ala	Lys	Val	Leu	Ser	Pro	Glu	Ser	Lys	Gln	Ala	Arg	Ala	Asn
225					230					235					240
Ser	Phe	Val	Gly	Thr	Ala	Gln	Tyr	Val	Ser	Pro	Glu	Leu	Leu	Thr	Glu
				245					250					255	
Lys	Ser	Ala	Cys	Lys	Ser	Ser	Asp	Leu	Trp	Ala	Leu	Gly	Cys	Ile	Ile
			260					265					270		
Tyr	Gln	Leu	Val	Ala	Gly	Leu	Pro	Pro	Phe	Arg	Ala	Gly	Asn	Glu	Tyr
		275					280					285			
Leu	Ile	Phe	Gln	Lys	Ile	Ile	Lys	Leu	Glu	Tyr	Asp	Phe	Pro	Glu	Lys
	290					295					300				
Phe	Phe	Pro	Lys	Ala	Arg	Asp	Leu	Val	Glu	Lys	Leu	Leu	Val	Leu	Asp
305					310					315					320
Ala	Thr	Lys	Arg	Leu	Gly	Cys	Glu	Glu	Met	Glu	Gly	Tyr	Gly	Pro	Leu
				325					330					335	
Lys	Ala	His	Pro	Phe	Phe	Glu	Ser	Val	Thr	Trp	Glu	Asn	Leu	His	Gln
			340					345					350		
Gln	Thr	Pro	Pro	Lys	Leu	Thr	Ala	Tyr	Leu	Pro	Ala	Met	Ser	Glu	Asp
		355					360					365			
Asp	Glu	Asp	Cys	Tyr	Gly	Asn	Tyr	Asp	Asn	Leu	Leu	Ser	Gln	Phe	Gly
	370					375					380				
Cys	Met	Gln	Val	Ser	Ser	Ser	Ser	Ser	Ser	His	Ser	Leu	Ser	Ala	Ser
385					390					395					400
Asp	Thr	Gly	Leu	Pro	Gln	Arg	Ser	Gly	Ser	Asn	Ile	Glu	Gln	Tyr	Ile
				405					410					415	
His	Asp	Leu	Asp	Ser	Asn	Ser	Phe	Glu	Leu	Asp	Leu	Gln	Phe	Ser	Glu
			420					425					430		
Asp	Glu	Lys	Arg	Leu	Leu	Leu	Glu	Lys	Gln	Ala	Gly	Gly	Asn	Pro	Trp
		435					440					445			
His	Gln	Phe	Val	Glu	Asn	Asn	Leu	Ile	Leu	Lys	Met	Gly	Pro	Val	Asp
	450					455					460				
Lys	Arg	Lys	Gly	Leu	Phe	Ala	Arg	Arg	Arg	Gln	Leu	Leu	Leu	Thr	Glu
465					470					475					480
Gly	Pro	His	Leu	Tyr	Tyr	Val	Asp	Pro	Val	Asn	Lys	Val	Leu	Lys	Gly

	485		490		495
Glu Ile Pro Trp Ser Gln Glu Leu Arg Pro Glu Ala Lys Asn Phe Lys	500		505		510
Thr Phe Phe Val His Thr Pro Asn Arg Thr Tyr Tyr Leu Met Asp Pro	515		520		525
Ser Gly Asn Ala His Lys Trp Cys Arg Lys Ile Gln Glu Val Trp Arg	530		535		540
Gln Arg Tyr Gln Ser His Pro Asp Ala Ala Val Gln	545		550		555

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATGGCCAGGA CCACCAGCCA GCTGTATGAC GCCGTGCCCA TCCAGTCCAG CGTGGTGTTA	60
TGTTCTTGCC CATCCCCATC AATGGTGAGG ACCCAGACTG AGTCCAGCAC GCCCCCTGGC	120
ATTCCTGGTG GCAGCAGGCA GGGCCCCGCC ATGGACGGCA CTGCAGCCGA GCCTCGGCCC	180
GGCGCCGGCT CCCTGCAGCA TCCAGCCTC CGCCGCAGCC TCGGAAGAAG CGGCCTGAGG	240
ACTTCAAGTT TGGGAAAATC CTTGGGGAAG GCTCTTTTTC CACGGTTGTC CTGGCTCGAG	300
AACTGGCAAC CTCCAGAGAA TATGCGATTA AAATTCTGGA GAAGCGACAT ATCATAAAAG	360
AGAACAAGGT CCCCTATGTA ACCAGAGAGC GGGATGTCAT GTCGCGCCTG GATCACCCTT	420
TCTTTGTTAA GCTTTACTTC ACATTTTCAGG ACGACGAGAA GCTGTATTTC GGCCTTAGTT	480
ATGCCAAAAA TGGAGAACTA CTTAAATATA TTCGCAAAT CGGTTTCATTC GATGAGACCT	540
GTACCCGATT TTACACGGCT GAGATCGTGT CTGCTTTAGA GTACTTGCAC GGCAAGGGCA	600

TCATTCACAG	GGACCTTAAA	CCGGAAAACA	TTTTGT TAAA	TGAAGATATG	CACATCCAGA	660
TCACAGATTT	TGGAACAGCA	AAAGTCTTAT	CCCCAGAGAG	CAAACAAGCC	AGGGCCAACT	720
CATTCGTGGG	AACAGCGCAG	TACGTTTCTC	CAGAGCTGCT	CACGGAGAAG	TCCGCCTGTA	780
AGAGTTCAGA	CCTTTGGGCT	CTTGATGCA	TAATATACCA	GCTTGTGGCA	GGA CTCCAC	840
CATTCCGAGC	TGGAAACGAG	TATCTTATAT	TTCAGAAGAT	CATTAAGTTG	GAATATGACT	900
TTCCAGAAAA	ATTCTTCCCT	AAGGCAAGAG	ACCTCGTGGA	GAAACTTTTG	GTTTTAGATG	960
CCACAAAGCG	GTTAGGCTGT	GAGGAAATGG	AAGGATACGG	ACCTCTTAAA	GCACACCCGT	1020
TCTTCGAGTC	CGTCACGTGG	GAGAACCTGC	ACCAGCAGAC	GCCTCCGAAG	CTCACCGCTT	1080
ACCTGCCGGC	TATGTCGGAA	GACGACGAGG	ACTGCTATGG	CAATTATGAC	AATCTCCTGA	1140
GCCAGTTTGG	CTGCATGCAG	GTGTCTTCGT	CCTCCTCCTC	ACACTCCCTG	TCAGCCTCCG	1200
ACACGGGCCT	GCCCCAGAGG	TCAGGCAGCA	ACATAGAGCA	GTACATTCAC	GATCTGGACT	1260
CGAACTCCTT	TGAACTGGAC	TTACAGTTTT	CCGAAGATGA	GAAGAGGTTG	TTGTTGGAGA	1320
AGCAGGCTGG	CGGAAACCCT	TGGCACCAGT	TTGTAGAAAA	TAATTTAATA	CTAAAGATGG	1380
GCCCAGTGGA	TAAGCGGAAG	GGTTTATTTG	CAAGACGACG	ACAGCTGTTG	CTCACAGAAG	1440
GACCACATTT	ATATTATGTG	GATCCTGTCA	ACAAAGTTCT	GAAAGGTGAA	ATTCCTTGGT	1500
CACAAGA ACT	TCGACCAGAG	GCCAAGAATT	TAAAACTTT	CTTTGTCCAC	ACGCCTAACA	1560
GGACGTATTA	TCTGATGGAC	CCCAGCGGGA	ACGCACACAA	GTGGTGCAGG	AAGATCCAGG	1620
AGGTTTGGAG	GCAGCGATAC	CAGAGCCACC	CGGACGCCGC	TGTGCAGTGA		1670

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Ala	Asn	Ser	Phe	Val	Gly	Thr	Ala	Gln	Tyr	Val	Ser	Pro	Glu	Leu	Leu
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Ala	Gly	Asn	Glu	Tyr	Leu	Ile	Phe	Gln	Lys
1				5					10

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Leu	Asp	His	Pro	Phe	Phe	Val	Lys
1				5			

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Arg	Gln	Arg	Tyr	Gln	Ser	His	Pro	Asp	Ala	Ala	Val	Gln
1				5					10			

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Leu	Ser	Pro	Glu	Ser	Lys	Gln	Ala	Arg	Ala	Asn	Ser
1				5					10		

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Thr	Ala	Ser	Gly	Val	Ala	Glu	Thr	Thr	Asn	Cys
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Arg	Pro	Arg	Ala	Ala	Thr	Phe
1				5		

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Thr Thr Tyr Ala Asp Phe Ile Ala Ser Gly Arg Thr Gly Arg Arg Asn
1 5 10 15

Ala Ile His Asp
20

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Ala His Pro Phe Phe Glu Ser Val Thr Trp Glu Asn Leu His Gln Gln
1 5 10 15

Thr Pro Pro Lys
20

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Ser Gly Ser Asn Ile Glu Gln Tyr Ile His Asp Leu Asp Ser Asn Ser
1 5 10 15

Phe Glu Leu Asp Leu
20

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Gln Ala Gly Gly Asn Pro Trp His Gln Phe Val Glu Asn Asn Leu Ile
1 5 10 15

Leu Lys

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Gln Leu Leu Leu Thr Glu Gly Pro His Leu Tyr Tyr Val Asp Pro Val
1 5 10 15

Asn Lys

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Thr	Phe	Phe	Val	His	Thr	Pro	Asn	Arg
1				5				

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Tyr	Gln	Ser	His	Pro	Asp	Ala	Ala	Val	Gln
1				5					10

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PCR PRIMER"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TTGAGCCAGT TTGGCTGC

18

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PCR PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

ACGTCCTGTT AGGCGTGTGG

20

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PCR PRIMER"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TTTGTGKGNA CNGCNCARTA YGT

23

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR PRIMER"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TTNACRAARA ANGGRTGRTC

20

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR PRIMER"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

AAYGARTAYY TNATHTTYCA RAA

23

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR PRIMER"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TCGGAGATCT GCCACCATGG AGCAGAAGCT GATCTCTGAA GAGGACTTGG ACGGCACTGC 60
AGCCGAGCCT CGG 73

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PCR PRIMER"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

GCGGGGTACC TCACTGCACA GCGGCGTCCG GGTG 34

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PCR PRIMER"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GCGGAGATCT GCCACCATGG AGCAGAAGCT GATCTCTGAA GAGGACTTGG CCAGGACCAC 60
CAGCCAGCTG TATGACG 77

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PCR PRIMER"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GCGGGGTACC TCAGTGCCAA GGGTTTCCGC CAGCCTGCTT

40

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PCR PRIMER"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

CGGGATCCAT GGA CTTC CGG TCGGGCTCA

29

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 419 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TGAGTCCAGC	ACGCCCCCTG	NATTTCTG	TGGCAGCAGG	CANGGGCCCG	CATGGACGGC	60
ACTGCAGCCG	AGCCTCGNCC	AGGGCCGGCA	TCCCATGCAG	CATGCCAGCC	TCCGCCGCAG	120
CTCGGAAGAA	GCGGCCTGAG	GA CTT CAAGT	TTGGGAAAAT	CTTGGGGAAG	GCTCTTTTNC	180
ACGGTTGTCT	GGCTCGAGAA	CTGGCAACCT	CCAGAGAATA	TGCGATTAAA	ATNCTGGAGA	240
AGCGACATAT	CATAAAAGAG	AACAAGGTCC	CTATGTAACC	AGAGANTGGG	ATGTCATGTC	300
GCGCCTGGAT	CACCCCTTCT	TTGTTAAGCT	T TA CTTCACA	TTTCAGGACG	ACGAGAAGNT	360
G TATTT CGGC	CTTAGTTATG	CNAAAAATTG	GAGAACTACT	TAAATATATT	CGCAAAATC	419

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 548 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

TTAAATAAAA	ATGCTGCAAG	GTTTCCGCCT	CTGCGTTCCC	CTTGTGATGG	CTGGCAGGTG	60
GTCTGGAAGC	GTCCCGGATG	GCGGCCAAGC	CGGCGAGGGG	CAGGTGTCCT	GGCAGCGAAG	120
GGCAGCCCGG	CCGCACNCGA	TCACTGCACA	GCGGCGTCCG	GGTGGCTCTG	GTATCGCTGC	180
CTCCAAACCT	CCTGGATCTT	CCTGCACCAC	TTGTGTGCGT	TCCCGCTGGG	GTCCATCAGA	240
TAATACGTCC	TGTTAGGCGT	GTGGACAAAG	AAAGTTTTAA	AATTCTTGGC	CTCTGGTCNA	300
AGTTCTTGTG	ACCAAGGAAT	TTCACCTTTC	AGAACTTTGT	TGACAGGATC	CACATAATAT	360
AAATGTGGTC	CTCTGTGAGC	AACAGCTGTC	GTCGTCTTGC	AAATAAACCC	TTCCGCTTAT	420
CCACTGGGCC	CATCTTTAGT	ATTAAATTAT	TTTCTACAAA	CTGGTGNCNA	GGGTTTCCGC	480

NAGCCTGGCT TCTCCAACAA CAANCTCTTC TCATCTTCGG AAAACTGTAA GTCCAGTTCA 540
NAGGAGTT 548

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Drosophila

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Met	Ala	Lys	Glu	Lys	Ala	Ser	Ala	Thr	Val	Ser	Leu	Gly	Glu	Ser	Asn	1	5	10	15
Phe	Arg	Asp	Ile	Asn	Leu	Lys	Asp	Leu	Ala	Val	Val	Val	Glu	Ala	Ala	20	25	30	
Ser	Arg	Leu	His	His	Gln	Gln	Asn	Val	Cys	Gly	Cys	Gly	Ala	Val	Ser	35	40	45	
Ser	Thr	Glu	Asn	Asn	Asn	Asn	Ser	Arg	Tyr	Gly	Ser	Ser	Lys	Tyr	Leu	50	55	60	
Thr	Asn	Gly	His	Thr	Ser	Pro	Leu	Ala	Ala	Ala	Val	Ala	Ser	Asn	Ser	65	70	75	80
Ser	Ser	Val	Ala	Thr	Thr	Pro	His	Cys	Arg	Met	Leu	His	Asn	Cys	Ser	85	90	95	
Leu	Gln	Gln	Tyr	Gln	Asn	Asp	Ile	Arg	Gln	Gln	Thr	Glu	Ile	Leu	Asp	100	105	110	
Met	Leu	Arg	His	Glu	His	Gln	Gln	Gly	Tyr	Gln	Ser	Gln	Gln	Gln	Gln	115	120	125	
Gln	Gln	Pro	Gln	Gln	Gln	Gln	Glu	Gln	Gln	Gln	Gln	Gln	Glu	Gln	Ser	130	135	140	
Gln	Gln	Gln	Gln	Gln	Leu	Gln	Asn	Pro	Ala	Pro	Arg	Arg	Ser	Pro	Asn	145	150	155	160

Asp	Phe	Ile	Phe	Gly	Arg	Tyr	Ile	Gly	Glu	Gly	Ser	Tyr	Ser	Ile	Val	165	170	175
Tyr	Leu	Ala	Val	Asp	Ile	His	Ser	Arg	Arg	Glu	Tyr	Ala	Ile	Lys	Val	180	185	190
Cys	Glu	Lys	Arg	Leu	Ile	Leu	Arg	Glu	Arg	Lys	Gln	Asp	Tyr	Ile	Lys	195	200	205
Arg	Glu	Arg	Glu	Val	Met	His	Gln	Met	Thr	Asn	Val	Pro	Gly	Phe	Val	210	215	220
Asn	Leu	Ser	Cys	Thr	Phe	Gln	Asp	Ala	Arg	Ser	Leu	Tyr	Phe	Val	Met	225	230	235
Thr	Tyr	Ala	Arg	Lys	Gly	Asp	Met	Leu	Pro	Tyr	Ile	Asn	Arg	Val	Gly	245	250	255
Ser	Phe	Asp	Val	Ala	Cys	Thr	Arg	His	Tyr	Ala	Ala	Glu	Leu	Leu	Leu	260	265	270
Ala	Cys	Glu	His	Met	His	Arg	Arg	Asn	Val	Val	His	Arg	Asp	Leu	Lys	275	280	285
Pro	Glu	Asn	Ile	Leu	Leu	Asp	Glu	Asp	Met	His	Thr	Leu	Ile	Ala	Asp	290	295	300
Phe	Gly	Ser	Ala	Lys	Val	Met	Thr	Ala	His	Glu	Arg	Ala	Leu	Ala	Thr	305	310	315
Glu	His	Cys	Ser	Glu	Gln	Arg	Arg	Ser	Asn	Ser	Asp	Glu	Asp	Asp	Glu	325	330	335
Asp	Ser	Asp	Arg	Leu	Glu	Asn	Glu	Asp	Glu	Asp	Phe	Tyr	Asp	Arg	Asp	340	345	350
Ser	Glu	Glu	Leu	Asp	Asp	Arg	Asp	Asp	Glu	Gln	Gln	Gln	Glu	Glu	Met	355	360	365
Asp	Ser	Pro	Arg	His	Arg	Gln	Arg	Arg	Tyr	Asn	Arg	His	Arg	Lys	Ala	370	375	380
Ser	Phe	Val	Gly	Thr	Ala	Gln	Tyr	Val	Ser	Pro	Glu	Val	Leu	Gln	Asn	385	390	395
Gly	Pro	Ile	Thr	Pro	Ala	Ala	Asp	Leu	Trp	Ala	Leu	Gly	Cys	Ile	Val	405	410	415
Tyr	Gln	Met	Ile	Ala	Gly	Leu	Pro	Pro	Phe	Arg	Gly	Ser	Asn	Asp	Tyr	420	425	430
Val	Ile	Phe	Lys	Glu	Ile	Leu	Asp	Cys	Ala	Val	Asp	Phe	Pro	Gln	Gly	435	440	445

Phe	Asp	Lys	Asp	Ala	Glu	Asp	Leu	Val	Arg	Lys	Leu	Leu	Arg	Val	Asp
450						455					460				
Pro	Arg	Asp	Arg	Leu	Gly	Ala	Gln	Asp	Glu	Phe	Gly	Tyr	Tyr	Glu	Ser
465					470					475					480
Ile	Arg	Ala	His	Pro	Phe	Phe	Ala	Gly	Ile	Asp	Trp	Gln	Thr	Leu	Arg
				485					490					495	
Gln	Gln	Thr	Pro	Pro	Pro	Ile	Tyr	Pro	Tyr	Leu	Pro	Gly	Val	Ser	Gln
			500					505					510		
Asp	Glu	Asp	Phe	Arg	Ser	Ser	Tyr	Thr	Val	Pro	Gly	Asp	Leu	Glu	Pro
		515					520					525			
Gly	Leu	Asp	Glu	Arg	Gln	Ile	Ser	Arg	Leu	Leu	Ser	Ala	Glu	Leu	Gly
530						535					540				
Val	Gly	Ser	Ser	Val	Ala	Met	Pro	Val	Lys	Arg	Ser	Thr	Ala	Lys	Asn
545					550					555					560
Ser	Phe	Asp	Leu	Asn	Asp	Ala	Glu	Lys	Leu	Gln	Arg	Leu	Glu	Gln	Gln
				565					570					575	
Lys	Thr	Asp	Lys	Trp	His	Val	Phe	Ala	Asp	Gly	Glu	Val	Ile	Leu	Lys
			580					585					590		
Lys	Gly	Phe	Val	Asn	Lys	Arg	Lys	Gly	Leu	Phe	Ala	Arg	Lys	Arg	Met
		595					600					605			
Leu	Leu	Leu	Thr	Thr	Gly	Pro	Arg	Leu	Ile	Tyr	Ile	Asp	Pro	Val	Gln
610						615					620				
Met	Ile	Lys	Lys	Gly	Glu	Ile	Pro	Trp	Ser	Pro	Asp	Leu	Arg	Ala	Glu
625					630					635					640
Tyr	Lys	Asn	Phe	Lys	Ile	Phe	Phe	Val	His	Thr	Pro	Asn	Arg	Thr	Tyr
				645					650					655	
Tyr	Leu	Asp	Asp	Pro	Glu	Gly	Tyr	Ala	Ile	His	Trp	Ser	Glu	Ala	Ile
			660					665					670		
Glu	Asn	Met	Arg	Lys	Leu	Ala	Tyr	Gly	Asp	Pro	Ser	Ser	Thr	Ser	Ala
		675					680					685			
Val	Ser	Cys	Ser	Ser	Gly	Ser	Ser	Asn	Ser	Leu	Ala	Val	Ile	Ser	Asn
	690					695					700				
Ser	Ser	Ala	Ala	Ser	Ser	Ser	Asn	Ser	Pro	Thr	Val	Lys	Arg	Ser	Ser
705					710					715					720
Pro	Val	Asn	Ala	Pro	Gln	Ala	Ser	Thr	Ala	Ser	Asp	Asn	Arg	Thr	Leu
				725					730					735	

Gly Ser Thr Arg Thr Gly Thr Ser Pro Ser Lys Lys Thr Ala Ser Lys
740 745 750

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Lys Met Gly Pro Val Asp Lys Arg Lys Gly Leu Phe Ala Arg Arg Arg
1 5 10 15
Gln Leu Leu Leu Thr Glu Gly Pro His Leu Tyr Tyr Val Asp Pro Val
20 25 30
Asn Lys Val Leu Lys Gly Glu Ile Pro Trp Ser Gln Glu Leu Arg Pro
35 40 45
Glu Ala Lys Asn Phe Lys Thr Phe Phe Val His Thr Pro Asn Arg Thr
50 55 60
Tyr Tyr Leu Met Asp Pro Ser Gly Asn Ala His Lys Trp Cys Arg Lys
65 70 75 80
Ile Gln Glu Val Trp Arg Gln Arg Tyr Gln Ser His
85 90

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Lys	Lys	Gly	Phe	Val	Asn	Lys	Arg	Lys	Gly	Leu	Phe	Ala	Arg	Lys	Arg	
1				5					10					15		
Met	Leu	Leu	Leu	Thr	Thr	Gly	Pro	Arg	Leu	Ile	Tyr	Ile	Asp	Pro	Val	
			20					25					30			
Gln	Met	Ile	Lys	Lys	Gly	Glu	Ile	Pro	Trp	Ser	Pro	Asp	Leu	Arg	Ala	
		35					40					45				
Glu	Tyr	Lys	Asn	Phe	Lys	Ile	Phe	Phe	Val	His	Thr	Pro	Asn	Arg	Thr	
	50					55					60					
Tyr	Tyr	Leu	Asp	Asp	Pro	Glu	Gly	Tyr	Ala	Ile	His	Trp	Ser	Glu	Ala	
65					70					75					80	
Ile	Glu	Asn	Met	Arg	Lys	Leu	Ala	Tyr	Gly	Asp	Pro					
				85					90							

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Arg	Glu	Gly	Tyr	Leu	Val	Lys	Lys	Gly	Ser	Val	Phe	Asn	Thr	Trp	Lys	
1				5					10					15		
Pro	Met	Trp	Val	Val	Leu	Leu	Glu	Asp	Gly	Ile	Glu	Phe	Tyr	Lys	Lys	
			20					25					30			
Lys	Ser	Asp	Asn	Ser	Pro	Lys	Gly	Met	Ile	Pro	Leu	Lys	Gly	Ser	Thr	
		35					40					45				

Leu Thr Ser Pro Cys Gln Asp Phe Gly Lys Arg Met Phe Val Phe Lys
50 55 60
Ile Thr Thr Thr Lys Gln Gln Asp His Phe Phe Gln Ala Ala Phe Leu
65 70 75 80
Glu Glu Arg Asp Ala Trp Val Arg Asp Ile Asn Lys Ala Ile Lys Cys
85 90 95
Ile Glu Gly Leu Glu
100

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Met Glu Gly Phe Leu Asn Arg Lys His Glu Trp Glu Ala His Asn Lys
1 5 10 15
Lys Ala Ser Ser Arg Ser Trp His Asn Val Tyr Gly Val Ile Asn Asn
20 25 30
Gln Glu Met Gly Phe Tyr Lys Asp Ala Lys Ser Ala Ala Ser Gly Ile
35 40 45
Pro Tyr His Ser Glu Val Pro Val Ser Leu Lys Glu Ala Ile Cys Glu
50 55 60
Val Ala Leu Asp Tyr Lys Lys Lys Lys His Val Phe Lys Leu Arg Leu
65 70 75 80
Ser Asp Gly Asn Glu Tyr Leu Phe Gln Ala Lys Asp Asp Glu Glu Met
85 90 95
Asn Thr Trp Ile Gln Ala Ile Ser Ser Ala Ile Ser Ser Asp Lys His
100 105 110

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Arg	Lys	Gly	Trp	Leu	Thr	Ile	Asn	Asn	Ile	Gly	Ile	Met	Lys	Gly	Gly	
1				5					10					15		
Ser	Lys	Glu	Tyr	Trp	Phe	Val	Leu	Thr	Ala	Glu	Asn	Leu	Ser	Trp	Tyr	
			20					25					30			
Lys	Asp	Asp	Glu	Glu	Lys	Glu	Lys	Lys	Tyr	Met	Leu	Ser	Val	Asp	Asn	
		35					40					45				
Leu	Lys	Leu	Arg	Asp	Val	Glu	Lys	Gly	Phe	Met	Ser	Ser	Lys	His	Ile	
		50				55					60					
Phe	Ala	Leu	Phe	Asn	Thr	Glu	Gln	Arg	Asn	Val	Tyr	Lys	Asp	Tyr	Arg	
65					70				75						80	
Gln	Leu	Glu	Leu	Ala	Cys	Glu	Thr	Gln	Glu	Glu	Val	Asp	Ser	Trp	Lys	
				85					90					95		
Ala	Ser	Phe	Leu	Arg	Ala	Gly	Val	Tyr	Pro	Glu	Arg	Val				
			100					105								

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Lys Gly Ser Gln Leu Leu Lys Val Lys Ser Ser Ser Trp Arg Arg Glu
1 5 10 15

Arg Phe Tyr Lys Leu Gln Glu Asp Cys Lys Thr Ile Trp Gln Glu Ser
20 25 30

Arg Lys Val Met Arg Ser Pro Glu Ser Gln Leu Phe Ser Ile Glu Asp
35 40 45

Ile Gln Glu Val Arg Met Gly His Arg Thr Glu Gly Leu Glu Lys Phe
50 55 60

Ala Arg Asp Ile Pro Glu Asp Arg Cys Phe Ser Ile Val Phe Lys Asp
65 70 75 80

Gln Arg Asn Thr Leu Asp Ile Ala Pro Ser Pro Ala Asp Ala Gln His
85 90 95

Trp Val Gln Gly Leu Arg Lys Ile Ile His His Ser Gly Ser Met Asp
100 105 110

Gln Arg